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## IN THE CLAIMS

Amend the claims as follows.

Claims 1-40 (Canceled).

41. (Currently Amended) An isolated oligonucleotide molecule consisting of a nucleotide sequence represented by any of SEQ ID NOs: 2 to 13, or 33 to 38, or the RNA equivalents of said SEQ IDs wherein T is replaced by U, or the complementary nucleic acid of said SEQ IDs, wherein the isolated oligonucleotide molecule is capable of being used as a species specific probe in the detection of one of the following fungal pathogens: *Candida albicans*, *Candida parapsilosis*, *Candida tropicalis*, *Candida kefyr*, *Candida krusei*, *Candida glabrata*, and *Candida dubliniensis*.

42. (Canceled)

43. (Previously Amended) Method to detect and identify at least one *Candida* species in one single assay, including

- (i) releasing, isolating and / or concentrating the nucleic acids of the fungal pathogens possibly present in the sample,
- (ii) optionally, amplifying the Internal Transcribed Spacer region (ITS) of said nucleic acids with at least one fungal universal primer pair,

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- (iii) hybridising the nucleic acids of step (i) or (ii) with at least one of the oligonucleotide molecules of claim 41,
- (iv) detecting the hybridisation complexes formed in step (iii), and
- (v) identifying the *Candida* species present in said sample, based on the hybridisation complex formed.

44. (Previously Added) Method according to claim 43, wherein said fungal universal primer pair is chosen from the following group of primer pairs:

ITS5: GGAAGTAAAAGTCGTAACAAGG (SEQ ID NO:44) and

ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45),

ITS5: GGAAGTAAAAGTCGTAACAAGG (SEQ ID NO:44) and

ITS2: GCTGCGTTCTTCATCGATGC (SEQ ID NO:46),

ITS1: TCCGTAGGTGAACCTGCGG (SEQ ID NO:47) and

ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45),

ITS1: TCCGTAGGTGAACCTGCGG (SEQ ID NO:47) and

ITS2: GCTGCGTTCTTCATCGATGC (SEQ ID NO:46),

ITS3: GCATCGATGAAGAACGCAGC (SEQ ID NO:49) and

ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45).

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45. (Currently Amended) Method according to claim 43 wherein ~~wherein~~ the *Candida* species is *Candida albicans* and wherein the at least one oligonucleotide molecule of step (iii) is

chosen from among SEQ ID NOs:2, 3, 33, 34 and 35.

46. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida parapsilosis* and wherein the at least one oligonucleotide molecule of step (iii) is

chosen from among SEQ ID NOs:4 and 5.

47. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida tropicalis* and wherein the at least one oligonucleotide molecule of step (iii) is

chosen from among SEQ ID NOs:6 and 36.

48. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida kefyr* and wherein the at least one oligonucleotide molecule of step (iii) is

chosen from among SEQ ID NOs:7 and 8.

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49. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida krusei* and wherein the at least one oligonucleotide molecule of step (iii) is

chosen from among SEQ ID NOs:9 and 37.

50. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida glabrata* and wherein the oligonucleotide molecule of step (iii) is SEQ ID NO:10.

51. (Previously Amended) Method according to claim 43 wherein the *Candida* species is *Candida dubliniensis* and wherein the at least one oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs:11, 12, 13 and 38.

52. (Previously Amended) Method according to claim 43 wherein the at least one oligonucleotide molecule of step (iii) is immobilized to a solid support.

53. (Previously Added) Method according to claim 43, further enabling the detection and identification of at least one of the following fungal pathogens: *Aspergillus flavus*, *Aspergillus versicolor*, *Aspergillus nidulans*, *Aspergillus fumigatus*, *Cryptococcus neoformans* and / or *Pneumocystis carinii*, wherein the nucleic acids of step (i) or (ii) are further hybridized with at least one of the following species specific oligonucleotide

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probes: SEQ ID NOs: 14 to 32, and 39 to 43.

54. (Previously Amended) Method for the simultaneous detection and differentiation of at least two *Candida* species in one single assay, including

- (i) releasing, isolating and / or concentrating the nucleic acids of the fungal pathogens possibly present in the sample,
- (ii) optionally, amplifying the Internal Transcribed Spacer region (ITS) of said nucleic acids with at least one fungal universal primer pair,
- (iii) hybridising the nucleic acids of step (i) or (ii) with at least two of the oligonucleotide molecules of claim 41, under the same hybridization conditions,
- (iv) detecting the hybridisation complexes formed in step (iii), and

identifying the *Candida* species present in said sample, based on the hybridisation complex formed.

55. (Previously Added) Method according to claim 54, wherein said fungal universal primer pair is chosen from the following group of primer pairs:

ITS5: GGAAGTAAAAGTCGTAACAAGG (SEQ ID NO:44) and

ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45),

ITS5: GGAAGTAAAAGTCGTAACAAGG (SEQ ID NO:44) and

ITS2: GCTGCGTTCTTCATCGATGC (SEQ ID NO:46),

ITS1: TCCGTAGGTGAACCTGCGG (SEQ ID NO:47) and

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ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45),  
ITS1: TCCGTAGGTGAACCTGCGG (SEQ ID NO:47) and  
ITS2: GCTGCGTTCTTCATCGATGC (SEQ ID NO:48),  
ITS3: GCATCGATGAAGAACGCAGC (SEQ ID NO:49) and  
ITS4: TCCTCCGCTTATTGATATGC (SEQ ID NO:45).

56. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida albicans* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 2, 3, 33, 34 and 35.

57. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida parapsilosis* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 4 and 5.

58. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida tropicalis* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 6 and 36.

59. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida kefyr* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 7 and 8.

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60. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida krusei* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 9 and 37.

61. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida glabrata* and wherein one of the oligonucleotide molecule of step (iii) is SEQ ID NO 10.

62. (Previously Amended) Method according to claim 54 wherein one *Candida* species is *Candida dubliniensis* and wherein at least one of the oligonucleotide molecule of step (iii) is chosen from among SEQ ID NOs: 11, 12, 13 and 38.

63. (Previously Amended) Method according to claim 54 wherein the at least two oligonucleotide molecule of step (iii) are immobilized to a solid support.

64. (Currently Amended) A combination of at least two isolated oligonucleotide molecules consisting of at least two isolated nucleotide sequences represented by any of SEQ ID NOs: 2 to 13, or 33 to 38, or the RNA equivalents of said SEQ IDs wherein T is replaced by U, or the complementary nucleic acid of said SEQ IDs, wherein said at least two oligonucleotide molecules are functional as hybridization probes under

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identical hybridization conditions, wherein at least one of the isolated nucleotide sequences is capable of being used as a species specific probe in the detection of one of the following fungal pathogens: *Candida albicans*, *Candida parapsilosis*, *Candida tropicalis*, *Candida kefyr*, *Candida krusei*, *Candida glabrata*, and *Candida dubliniensis*.